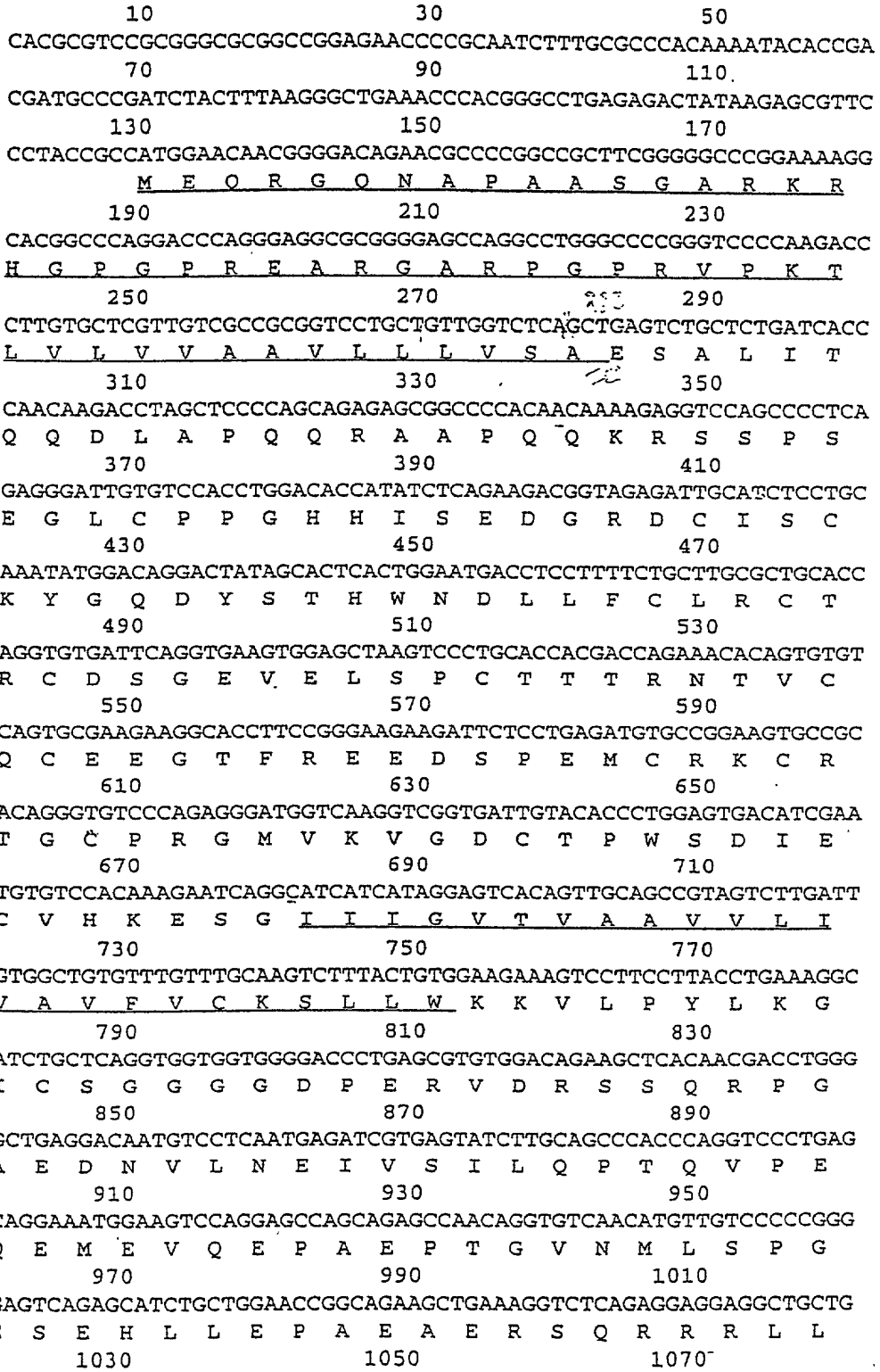
Figure 1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70 90 110
CGATGCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC
130 150 170
CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGCCCGGAAAAGG
M E Q R G Q N A P A A S G A R K R
190 210 230
CACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACC
H G P G P R E A R G A R P G P R V P K T
250 270 290
CTTGTGCTCGTTGTCGCCGCGGTCCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC
L V L V V A A V L L L V S A E S A L I T
310 330 350
CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAGGTCCAGCCCCTCA
Q Q D L A P Q Q R A A P Q Q K R S S P S
370 390 410
GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGC
E G L C P P G H H I S E D G R D C I S C
430 450 470
AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCGCTGCACC
K Y G Q D Y S T H W N D L L F C L R C T
490 510 530
AGGTGTGATTCAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT
R C D S G E V E L S P C T T T R N T V C
550 570 590
CAGTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC
Q C E E G T F R E E D S P E M C R K C R
610 630 650
ACAGGGTGTCCCAGAGGGATGGTCAAGGTCGGTGATTGTACACCCTGGAGTGACATCGAA
T G C P R G M V K V G D C T P W S D I E
670 690 710
TGTGTCCACAAAGAATCAGGCATCATCATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT
C V H K E S G I I I G V T V A A V V L I
730 750 770
GTGGCTGTGTTTGTTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTCCTTACCTGAAAGGC
V A V F V C K S L L W K K V L P Y L K G
790 810 830
ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGG
I C S G G G G D P E R V D R S S Q R P G
850 870 890
GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAG
A E D N V L N E I V S I L Q P T Q V P E
910 930 950
CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
Q E M E V Q E P A E P T G V N M L S P G
970 990 1010
GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
E S E H L L E P A E A E R S Q R R R L L
1030 1050 1070

Figure 1 (continued)

```
GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA
V  P  A  N  E  G  D  P  T  E  T  L  R  Q  C  F  D  D  F  A
      1090                1110                1130
GACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT
D  L  V  P  F  D  S  W  E  P  L  M  R  K  L  G  L  M  D  N
      1150                1170                1190
GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGTACACGATGCTG
E  I  K  V  A  K  A  E  A  A  G  H  R  D  T  L  Y  T  M  L
      1210                1230                1250
ATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG
I  K  W  V  N  K  T  G  R  D  A  S  V  H  T  L  L  D  A  L
      1270                1290                1310
GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA
E  T  L  G  E  R  L  A  K  Q  K  I  E  D  H  L  L  S  S  G
      1330                1350                1370
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA
K  F  M  Y  L  E  G  N  A  D  S  A  M  S  *
      1390                1410                1430
GGAAGTGAGACCTTCCCTGGTTTACCTTTTTTCTGGAAAAAGCCCAACTGGACTCCAGTC
      1450                1470                1490
AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAAACTCTCCCATCCAACA
      1510                1530                1550
TCACCCAGTGGATGGAACATCCTGTAACTTTTCACTGCACTTGGCATTATTTTTATAAGC
      1570                1590
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAAA
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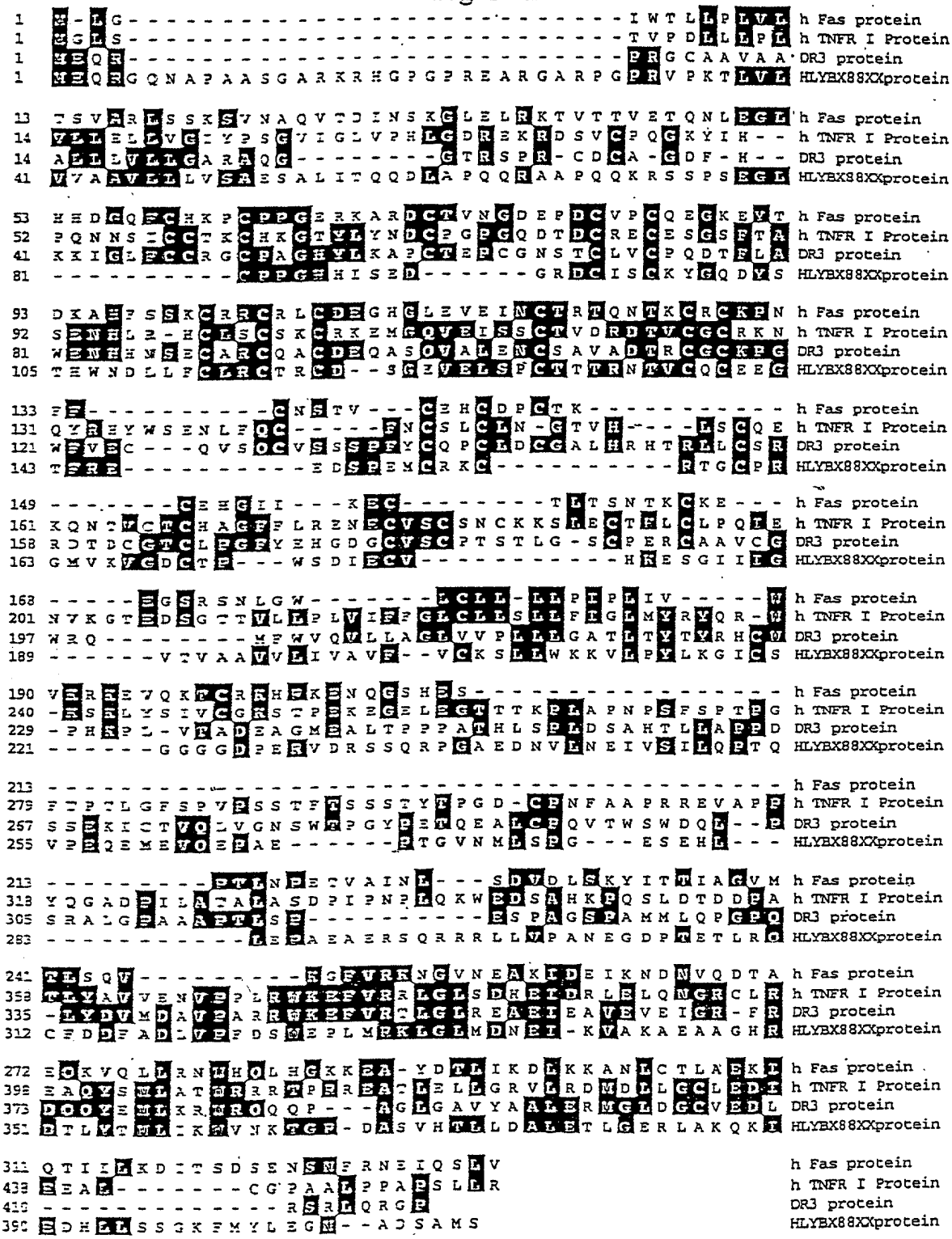
Figure 2



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Figure 3

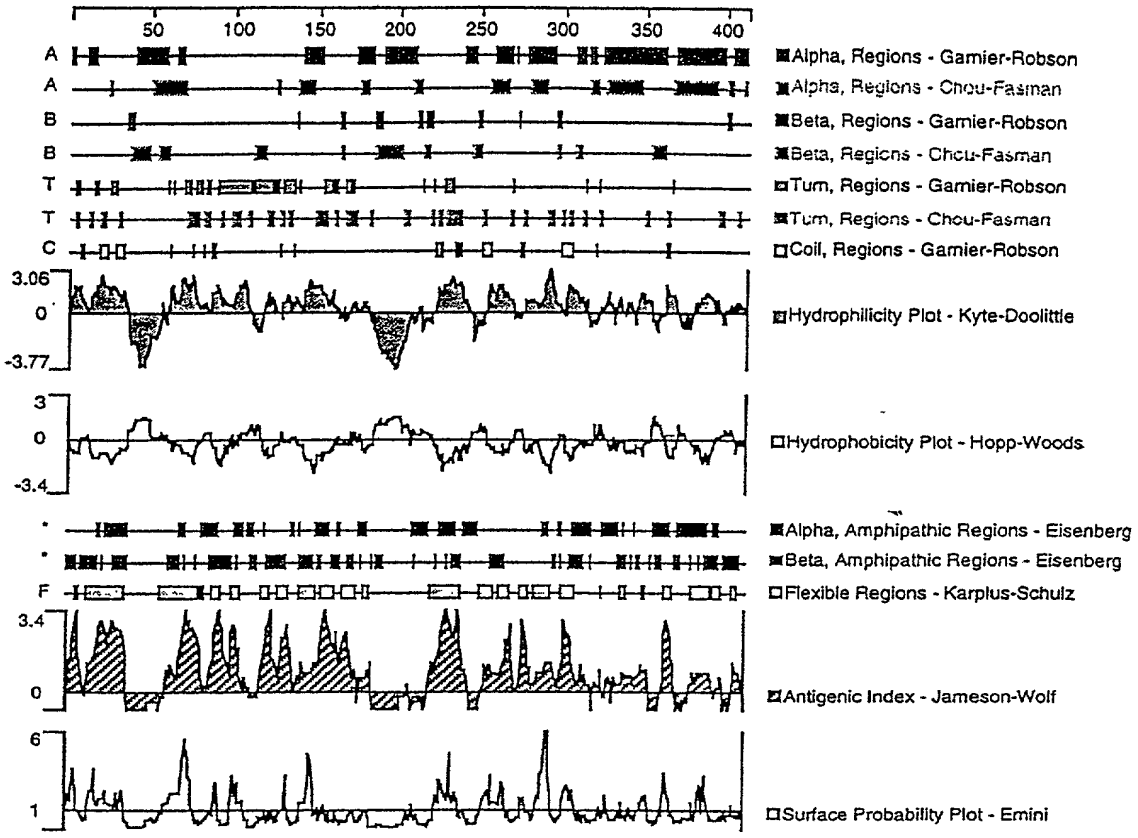

50
100
150
200
250
300
350
400
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
3.06
0
-3.77
Hydrophilicity Plot - Kyte-Doolittle
3
0
-3.4
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini

Figure 4

HAPBU13R

```
  1 AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT
 51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNTGG
```

HSBBU76R

```
  1 TTTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC
 51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTC CATAGNGTCC
151 TTATTATCAC ATTCAGCTTA TAAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT
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Figure 5

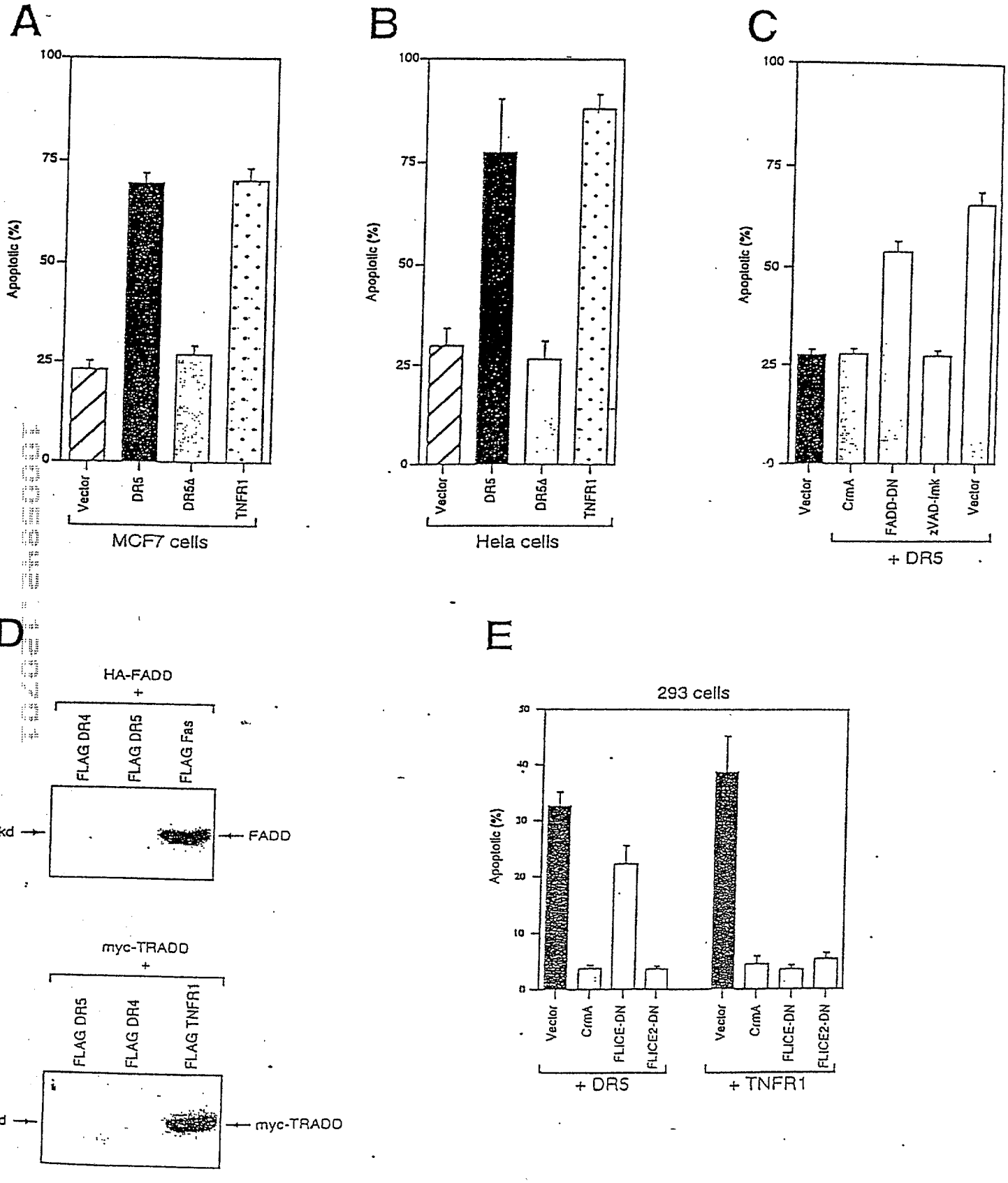
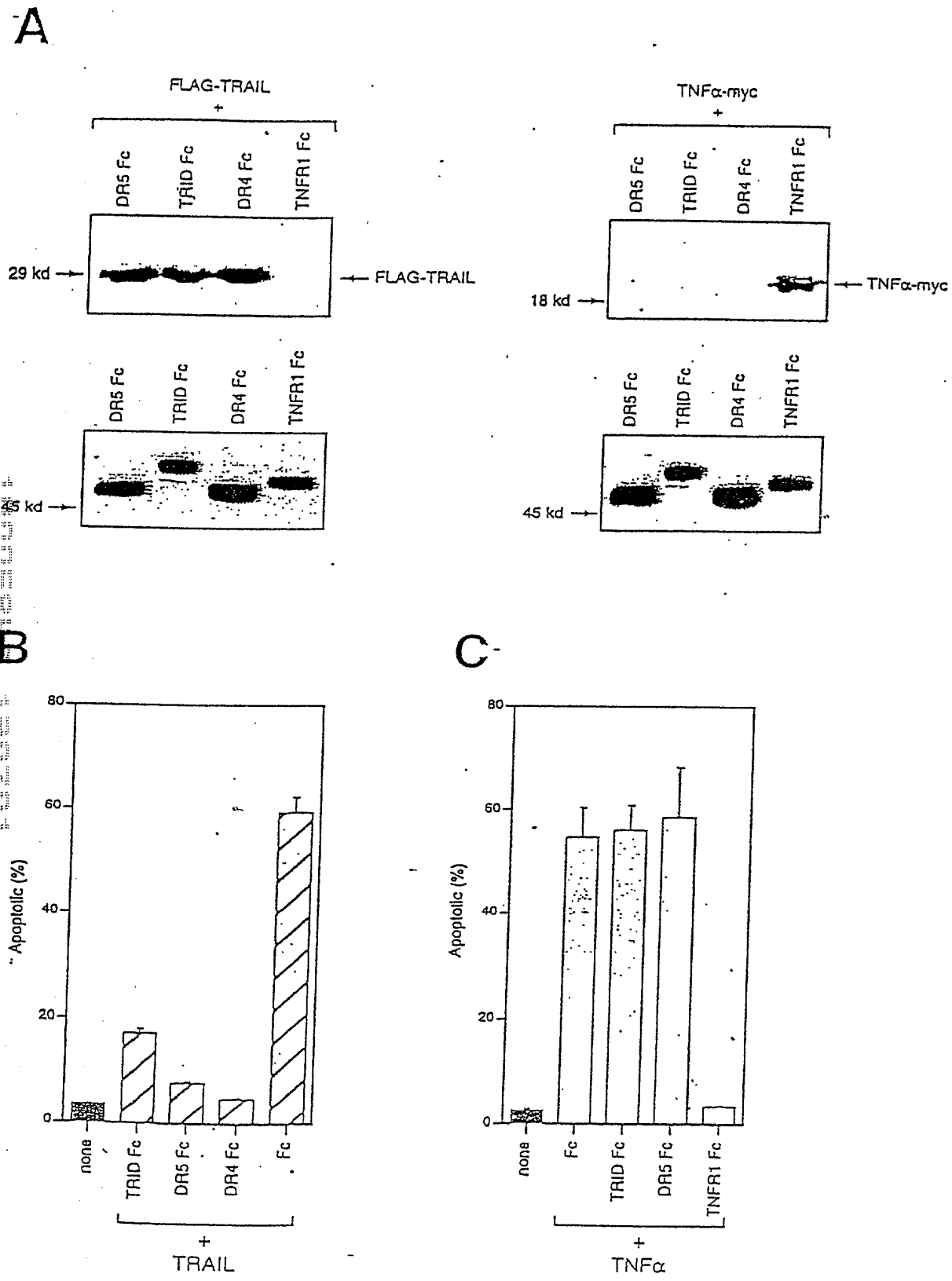

A
B
C
Apoptotic (%)
100
75
50
25
0
Vector
DR5
DR5Δ
TNFR1
MCF7 cells
Hela cells
CrmA
FADD-DN
zVAD-fmk
+ DR5
D
HA-FADD
+
FLAG DR4
FLAG DR5
FLAG Fas
29 kd
FADD
myc-TRADD
FLAG DR5
FLAG DR4
FLAG TNFR1
45 kd
myc-TRADD
E
293 cells
FLICE-DN
FLICE2-DN
+ TNFR1

Figure 6


A
FLAG-TRAIL
+
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
29 kd
FLAG-TRAIL
TNFα-myc
18 kd
TNFα-myc
45 kd
B
Apoptotic (%)
80
60
40
20
0
none
TRID Fc
DR5 Fc
DR4 Fc
Fc
TRAIL
C
Apoptotic (%)
Fc
TNFR1 Fc
TNFα